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Xu, Wenfeng  
Madden, Karen  
Yee, David P.

<130> 98-75

<151> 1999-01-07

<151> 1999-12-09

<170> FastSEQ for Windows Version 3.0

<211> 1192

<213> Homo sapiens

<221> CDS

$\langle 222 \rangle$  (6) ... (746)

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Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val  
1 5 10 15

gac cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag 98  
Asp Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys  
20 25 30

ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt 146  
Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys  
35 40 45

gga Gly	cag Gln	cac His 50	cct Pro	aag Lys	caa Gln	tgt Cys	gca Ala 55	tac Tyr	ttc Phe	tgt Cys	gag Glu	aac Asn 60	aag Lys	ctc Leu	agg Arg	194
agc Ser	cca Pro 65	gtg Val	aac Asn	ctt Leu	cca Pro	cca Pro 70	gag Glu	ctc Leu	agg Arg	aga Arg	cag Gln 75	cgg Arg	agt Ser	gga Gly	gaa Glu	242
gtt Val 80	gaa Glu	aac Asn	aat Asn	tca Ser	gac Asp 85	aac Asn	tcg Ser	gga Gly	agg Arg	tac Tyr 90	caa Gln	gga Gly	ttg Leu	gag Glu	cac His 95	290
aga Arg	ggc Gly	tca Ser	gaa Glu	gca Ala 100	agt Ser	cca Pro	gct Ala	ctc Leu	ccg Pro 105	ggg Gly	ctg Leu	aag Lys	ctg Leu	agt Ser 110	gca Ala	338
gat Asp	cag Gln	gtg Val	gcc Ala 115	ctg Leu	gtc Val	tac Tyr	agc Ser	acg Thr	ctg Leu 120	ggg Gly	ctc Leu	tgc Cys	ctg Leu 125	tgt Cys	gcc Ala	386
gtc Val	ctc Leu	tgc Cys 130	tgc Cys	ttc Phe	ctg Leu	gtg Val	gcg Ala 135	gtg Val	gcc Ala	tgc Cys	ttc Phe	ctc Leu 140	aag Lys	aag Lys	agg Arg	434
ggg Gly	gat Asp 145	ccc Pro	tgc Cys	tcc Ser	tgc Cys	cag Gln 150	ccc Pro	cgc Arg	tca Ser	agg Arg	ccc Pro 155	cgt Arg	caa Gln	agt Ser	ccg Pro	482
gcc Ala 160	aag Lys	tct Ser	tcc Ser	cag Gln	gat Asp 165	cac His	gcg Ala	atg Met	gaa Glu	gcc Ala 170	ggc Gly	agc Ser	cct Pro	gtg Val	agc Ser 175	530
aca Thr	tcc Ser	ccc Pro	gag Glu	cca Pro 180	gtg Val	gag Glu	acc Thr	tgc Cys	agc Ser 185	ttc Phe	tgc Cys	ttc Phe	cct Pro	gag Glu 190	tgc Cys	578
agg Arg	gcg Ala	ccc Pro	acg Thr 195	cag Gln	gag Glu	agc Ser	gca Ala 200	gtc Val	acg Thr	cct Pro	ggg Gly	acc Thr 205	ccc Pro	gac Asp	ccc Pro	626
act Thr	tgt Cys	gct Ala 210	gga Gly	agg Arg	tgg Trp	ggg Gly	tgc Cys 215	cac His	acc Thr	agg Arg	acc Thr 220	aca Thr	gtc Val	ctg Leu	cag Gln	674

Met 1	Ser	Gly	Leu	Gly 5	Arg	Ser	Arg	Arg	Gly 10	Gly	Arg	Ser	Arg	Val 15	Asp
Gln	Glu	Glu	Arg	Trp	Ser	Leu	Ser	Cys 25	Arg	Lys	Glu	Gln	Gly 30	Lys	Phe
Tyr	Asp	His 35	Leu	Leu	Arg	Asp	Cys 40	Ile	Ser	Cys	Ala	Ser	Ile	Cys	Gly
Gln	His 50	Pro	Lys	Gln	Cys	Ala 55	Tyr	Phe	Cys	Glu	Asn 60	Lys	Leu	Arg	Ser
Pro 65	Val	Asn	Leu	Pro	Pro 70	Glu	Leu	Arg	Arg	Gln 75	Arg	Ser	Gly	Glu	Val 80
Glu	Asn	Asn	Ser	Asp 85	Asn	Ser	Gly	Arg	Tyr 90	Gln	Gly	Leu	Glu	His 95	Arg
Gly	Ser	Glu	Ala 100	Ser	Pro	Ala	Leu	Pro 105	Gly	Leu	Lys	Leu	Ser	Ala	Asp
Gln	Val	Ala 115	Leu	Val	Tyr	Ser	Thr 120	Leu	Gly	Leu	Cys	Leu	Cys	Ala	Val
Leu	Cys 130	Cys	Phe	Leu	Val 135	Ala	Val	Ala	Cys	Phe	Leu	Lys	Lys	Arg	Gly
Asp 145	Pro	Cys	Ser	Cys 150	Gln	Pro	Arg	Ser	Arg	Pro 155	Arg	Gln	Ser	Pro	Ala 160
Lys	Ser	Ser	Gln 165	Asp	His	Ala	Met	Glu	Ala 170	Gly	Ser	Pro	Val	Ser	Thr
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<210> 3
<211> 360
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(360)

<400> 3

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Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe  
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tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga 144  
Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly  
35 40 45

cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc 192  
Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser  
50 55 60

cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt 240  
Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val  
65 70 75 80

gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga 288  
Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg  
85 90 95

ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt qca qat 336

360

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<210> 4
<211> 120
<212> PRT
<213> Homo sapiens
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<210> 5
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<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (14)...(895)
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Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly	
15 20 25	
gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg	145
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu	
30 35 40	
ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc	193
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg	
45 50 55 60	
acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc	241
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly	
65 70 75	
aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc	289
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile	
80 85 90	
tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc	337
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu	
95 100 105	
agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga	385
Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly	
110 115 120	
gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag	433
Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu	
125 130 135 140	
cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt	481
His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser	
145 150 155	
gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt	529
Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys	
160 165 170	
gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag	577
Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys	
175 180 185	
agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt	625

004070-9595460

Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser	
190 195 200	
ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg	673
Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val	
205 210 215 220	
agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag	721
Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu	
225 230 235	
tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac	769
Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp	
240 245 250	
ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg	817
Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu	
255 260 265	
cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg	865
Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val	
270 275 280	
cct gcc cag gag ggg ggc cca ggt gca taa atgggggtca gggagggaaa	915
Pro Ala Gln Glu Gly Gly Pro Gly Ala *	
285 290	
ggaggagggga gagagatgga gaggagggga gagagaaaga gaggtgggga gaggggagag	975
agatatgagg agagagagac agaggaggca gaaagggaga gaaacagagg agacagagag	1035
ggagagagag acagagggag agagagacag aggggaagag aggcagagag ggaaagaggc	1095
agagaaggaa agagacaggc agagaaggag agaggcagag agggagagag gcagagaggg	1155
agagaggcag agagacagag agggagagag ggacagagag agatagagca ggaggtcggg	1215
gcactctgag tcccagttcc cagtgcagct gtaggtcgtc atcacctaac cacacgtgca	1275
ataaagtcct cgtgcctgct gctcacagcc cccgagagcc cctcctcctg gagaataaaa	1335
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<210> 6  
 <211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
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Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg

20 25 30  
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met  
 35 40 45  
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala  
 50 55 60  
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp  
 65 70 75 80  
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His  
 85 90 95  
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val  
 100 105 110  
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn  
 115 120 125  
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser  
 130 135 140  
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val  
 145 150 155 160  
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys  
 165 170 175  
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro  
 180 185 190  
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser  
 195 200 205  
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro  
 210 215 220  
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro  
 225 230 235 240  
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala  
 245 250 255  
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro  
 260 265 270  
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu  
 275 280 285  
 Gly Gly Pro Gly Ala  
 290

<210> 7  
 <211> 995  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (219)...(773)



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agctgctctt	gctgcatttg	ctctggaatt	cttgtagaga	tattacttgt	ccttccaggc	180
tgttctttct	gtagctccct	tgttttcttt	ttgtgatac	atg ttg cag atg gct ggg		236
			Met Leu Gln Met Ala Gly			
			1	5		

cag tgc tcc caa aat gaa tat ttt gac agt ttg ttg cat gct tgc ata 284  
Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile  
10 15 20

cct tgt caa ctt cga tgt tct tct aat act cct cct cta aca tgt cag 332  
Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln  
25 30 35

cgt tat tgt aat gca agt gtg acc aat tca gtg aaa gga acg aat gcg 380  
Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala  
40 45 50

att ctc tgg acc tgt ttg gga ctg agc tta ata att tct ttg gca gtt 428  
Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu Ile Ile Ser Leu Ala Val  
55 60 65 70

ttc gtg cta atg ttt ttg cta agg aag ata agc tct gaa cca tta aag 476  
Phe Val Leu Met Phe Leu Leu Arg Lys Ile Ser Ser Glu Pro Leu Lys  
75 80 85

gac gag ttt aaa aac aca gga tca ggt ctc ctg ggc atg gct aac att 524  
Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu Leu Gly Met Ala Asn Ile  
90 95 100

gac ctg gaa aag agc agg act ggt gat gaa att att ctt ccg aga ggc 572  
Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu Ile Ile Leu Pro Arg Gly  
105 110 115

ctc gag tac acg gtg gaa gaa tgc acc tgt gaa gac tgc atc aag agc 620  
Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys Glu Asp Cys Ile Lys Ser  
120 125 130

aaa ccg aag gtc gac tct gac cat tgc ttt cca ctc cca gct atg gag 668  
Lys Pro Lys Val Asp Ser Asp His Cys Phe Pro Leu Pro Ala Met Glu  
135 140 145 150

gaa ggc gca acc att ctt gtc acc acg aaa acg aat gac tat tgc aag 716





<220>  
<223> Motif describing the cysteine-rich pseudo-repeat domain

<221> VARIANT  
<222> (1)...(2)  
<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT  
<222> (4)...(4)  
<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT  
<222> (5)...(5)  
<223> Xaa is glutamine, glutamic acid, or lysine.

<221> VARIANT  
<222> (6)...(6)  
<223> Xaa is glutamine, glutamic acid, lysine, asparagine, arginine, aspartic acid, histidine, or serine.

<221> VARIANT  
<222> (7)...(7)  
<223> Xaa is glutamine or glutamic acid.

<221> VARIANT  
<222> (8)...(9)  
<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT  
<222> (10)...(11)  
<223> Xaa is tyrosine, phenylalanine, or tryptophan.

<221> VARIANT  
<222> (13)...(13)  
<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT  
<222> (16)...(17)  
<223> Each Xaa is independently any amino acid residue

except cysteine.

<221> VARIANT

<222> (19)...(19)

<223> Xaa is isoleucine, methionine, leucine, or valine.

<221> VARIANT

 $\langle 222 \rangle \quad (20) \dots (20)$ 

<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT

<222> (22) ... (24)

<223> Each Xaa is independently any amino acid residue except cysteine.

<221> VARIANT

<222> (26)...(31)

<223> Each Xaa is independently any amino acid residue except cysteine.

<221> VARIANT

<222> (32) . . . (33)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

## <221> VARIANT

<222> (35) . . . (36)

<223> Each Xaa is independently any amino acid residue except cysteine.

## <221> VARIANT

 $\langle 222 \rangle \quad (37) \dots (37)$ 

<223> Xaa is tyrosine or phenylalanine.

## <221> VARIANT

<222> (39)...(40)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<400> 10

Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Leu	Leu	Xaa
1				5					10					15	
Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30	
Xaa	Cys	Xaa	Xaa	Xaa	Cys	Xaa	Xaa								

35

40

<210> 11  
 <211> 360  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide sequence encoding the polypeptide of SEQ ID NO:4

<221> variation

<222> (1)...(360)

<223> Each N is independently A, T, G, or C.

<400> 11

atgwsnggny	tnggnmgnws	nmgnmgnggn	ggnmgnwsnm	gngtngayca	rgargarmgn	60
tggwsnytnw	sntgymgnaa	rgarcarggn	aarttytayg	aycayytnyt	nmngnaytgy	120
athwsntgyg	cnwsnathtg	yggncarcay	ccnaarcart	gygcntaytt	ytgygaraay	180
aarytnmgnw	sncngtnaa	yytnccnccn	garytnmgnm	gncarmgnws	ngngargtn	240
garaayaayw	sngayaayws	nggnmgntay	carggnytn	arcaymgngg	nwsngargcn	300
wsnccngcny	tnccnggnyt	naarytnwsn	gcngaycarg	tngcnytngt	ntaywsnacb	360

<210> 12

<211> 741

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide sequence encoding a polypeptide of SEQ ID NO:2

<221> variation

<222> (1)...(741)

<223> Each N is independently A, T, G, or C.

<400> 12

atgwsnggny	tnggnmgnws	nmgnmgnggn	ggnmgnwsnm	gngtngayca	rgargarmgn	60
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athwsntgyg	cnwsnathtg	yggncarcay	ccnaarcart	gygcntaytt	ytgygaraay	180
aarytnmgnw	sncngtnaa	yytnccnccn	garytnmgnm	gncarmgnws	ngngargtn	240
garaayaayw	sngayaayws	nggnmgntay	carggnytn	arcaymgngg	nwsngargcn	300
wsnccngcny	tnccnggnyt	naarytnwsn	gcngaycarg	tngcnytngt	ntaywsnacb	360
ytnggnytn	gyytnytn	ngntnytn	tygtyytn	tngcngtngc	ntgyttyytn	420
aaraarmgng	gngayccntg	ywsntgycar	ccnmgnwsnm	gnccnmgnca	rwsnccngcn	480

aarwsnwsnc	argaycaygc	natggargcn	ggwnsnccng	tnwsnacnws	nccngarccn	540
gtngaracnt	gywsnttytg	ytyccngar	tgymgngcnc	cnacncarga	rwsngcngtn	600
acnccnggna	cncngaycc	nacntgygc	ggnmgtggg	gntgycayac	nmgnacnacn	660
gtnytncarc	cntgyccnca	yathccngay	wsnggnytn	gnathgtntg	ygtncnccngcn	720
cargarggng	gncnccngngc	n				741

<210> 13  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> FLAG tag

<400> 13  
 Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 14  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Glu-Glu tag

<400> 14  
 Glu Glu Tyr Met Pro Met Glu  
 1 5

<210> 15  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide ZC19980

<400> 15  
 cgaagagcag tactgggatc ctct 24

<210> 16  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

gag gaa gct cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca 526



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			85					90					95			
gct	cca	gga	gaa	ggc	aac	tcc	agt	cag	aac	agc	aga	aat	aag	cgt	gcc	574
Ala	Pro	Gly	Glu	Gly	Asn	Ser	Ser	Gln	Asn	Ser	Arg	Asn	Lys	Arg	Ala	
		100					105					110				
gtt	cag	ggt	cca	gaa	gaa	aca	gtc	act	caa	gac	tgc	ttg	caa	ctg	att	622
Val	Gln	Gly	Pro	Glu	Glu	Thr	Val	Thr	Gln	Asp	Cys	Leu	Gln	Leu	Ile	
	115					120					125					
gca	gac	agt	gaa	aca	cca	act	ata	caa	aaa	gga	tct	tac	aca	ttt	gtt	670
Ala	Asp	Ser	Glu	Thr	Pro	Thr	Ile	Gln	Lys	Gly	Ser	Tyr	Thr	Phe	Val	
130					135					140					145	
cca	tgg	ctt	ctc	agc	ttt	aaa	agg	gga	agt	gcc	cta	gaa	gaa	aaa	gag	718
Pro	Trp	Leu	Leu	Ser	Phe	Lys	Arg	Gly	Ser	Ala	Leu	Glu	Glu	Lys	Glu	
				150					155					160		
aat	aaa	ata	ttg	gtc	aaa	gaa	act	ggg	tac	ttt	ttt	ata	tat	ggt	cag	766
Asn	Lys	Ile	Leu	Val	Lys	Glu	Thr	Gly	Tyr	Phe	Phe	Ile	Tyr	Gly	Gln	
			165					170					175			
gtt	tta	tat	act	gat	aag	acc	tac	gcc	atg	gga	cat	cta	att	cag	agg	814
Val	Leu	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Met	Gly	His	Leu	Ile	Gln	Arg	
		180					185					190				
aag	aag	gtc	cat	gtc	ttt	ggg	gat	gaa	ttg	agt	ctg	gtg	act	ttg	ttt	862
Lys	Lys	Val	His	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu	Val	Thr	Leu	Phe	
		195				200					205					
cga	tgt	att	caa	aat	atg	cct	gaa	aca	cta	ccc	aat	aat	tcc	tgc	tat	910
Arg	Cys	Ile	Gln	Asn	Met	Pro	Glu	Thr	Leu	Pro	Asn	Asn	Ser	Cys	Tyr	
210					215					220					225	
tca	gct	ggc	att	gca	aaa	ctg	gaa	gaa	gga	gat	gaa	ctc	caa	ctt	gca	958
Ser	Ala	Gly	Ile	Ala	Lys	Leu	Glu	Glu	Gly	Asp	Glu	Leu	Gln	Leu	Ala	
				230					235					240		
ata	cca	aga	gaa	aat	gca	caa	ata	tca	ctg	gat	gga	gat	gtc	aca	ttt	1006
Ile	Pro	Arg	Glu	Asn	Ala	Gln	Ile	Ser	Leu	Asp	Gly	Asp	Val	Thr	Phe	
			245					250					255			
ttt	ggt	gca	ttg	aaa	ctg	ctg	tgac	tact	acac	cat	gtc	tgtag	ctatt			1057
Phe	Gly	Ala	Leu	Lys	Leu	Leu										

05479655-010700

260

ttctctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac caaaaaaaaa 1117  
 aaaaaaaaaa aaaaaaccct cgagcgccg cc 1149

&lt;210&gt; 18

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro  
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 Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu  
 20 25 30  
 Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val  
 35 40 45  
 Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly  
 50 55 60  
 His His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly  
 65 70 75 80  
 Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro  
 85 90 95  
 Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg  
 100 105 110  
 Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu  
 115 120 125  
 Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe  
 130 135 140  
 Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys  
 145 150 155 160  
 Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly  
 165 170 175  
 Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln  
 180 185 190  
 Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu  
 195 200 205  
 Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys  
 210 215 220  
 Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu  
 225 230 235 240  
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<220>  
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Met Ala Met Ala Phe	
1 5	
tgc ccc aaa gat cag tac tgg gac tcc tca agg aaa tcc tgt gtc tcc	164
Cys Pro Lys Asp Gln Tyr Trp Asp Ser Ser Arg Lys Ser Cys Val Ser	
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Cys Ala Leu Thr Cys Ser Gln Arg Ser Gln Arg Thr Cys Thr Asp Phe	
25 30 35	
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Cys Lys Phe Ile Asn Cys Arg Lys Glu Gln Gly Arg Tyr Tyr Asp His	
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ctc ctg ggg gcc tgc gtc agc tgt gac tcc acc tgc aca cag cac cct	308
Leu Leu Gly Ala Cys Val Ser Cys Asp Ser Thr Cys Thr Gln His Pro	
55 60 65	
cag cag tgt gcc cac ttc tgt gag aaa agg ccc aga agc cag gcg aac	356
Gln Gln Cys Ala His Phe Cys Glu Lys Arg Pro Arg Ser Gln Ala Asn	
70 75 80 85	
ctc cag ccc gag ctc ggg aga cca cag gcc ggg gag gtg gaa gtc agg	404
Leu Gln Pro Glu Leu Gly Arg Pro Gln Ala Gly Glu Val Glu Val Arg	
90 95 100	
tca gac aac tca gga agg cac cag gga tct gag cat ggt cca gga ttg	452
Ser Asp Asn Ser Gly Arg His Gln Gly Ser Glu His Gly Pro Gly Leu	
105 110 115	
agg cta agt agc gac cag ctg act ctc tac tgc aca ctg ggg gtc tgc	500

05473356.010700

Arg	Leu	Ser	Ser	Asp	Gln	Leu	Thr	Leu	Tyr	Cys	Thr	Leu	Gly	Val	Cys		
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ctc	tgc	gcc	atc	ttc	tgc	tgt	ttc	ttg	gtg	gcc	ttg	gcc	tcc	ttc	ctc	548	
Leu	Cys	Ala	Ile	Phe	Cys	Cys	Phe	Leu	Val	Ala	Leu	Ala	Ser	Phe	Leu		
	135					140					145						
agg	cgt	aga	gga	gag	cca	cta	ccc	agc	cag	cct	gcc	ggg	cca	cgt	ggg	596	
Arg	Arg	Arg	Gly	Glu	Pro	Leu	Pro	Ser	Gln	Pro	Ala	Gly	Pro	Arg	Gly		
150					155					160					165		
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Ser	Gln	Ala	Asn	Ser	Pro	His	Ala	His	Arg	Pro	Val	Thr	Glu	Ala	Cys		
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gac	gag	gtg	acc	gcg	tca	ccc	cag	cct	gtg	gaa	acg	tgt	agc	ttc	tgc	692	
Asp	Glu	Val	Thr	Ala	Ser	Pro	Gln	Pro	Val	Glu	Thr	Cys	Ser	Phe	Cys		
			185				190						195				
ttc	ccg	gag	cgc	agt	tct	ccc	act	cag	gag	agc	gcg	ccg	cgt	tcg	ctc	740	
Phe	Pro	Glu	Arg	Ser	Ser	Pro	Thr	Gln	Glu	Ser	Ala	Pro	Arg	Ser	Leu		
	200					205						210					
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Gly	Ile	His	Gly	Phe	Ala	Gly	Thr	Ala	Ala	Pro	Gln	Pro	Cys	Met	Arg		
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Ala	Thr	Val	Gly	Gly	Leu	Gly	Val	Leu	Arg	Ala	Ser	Thr	Gly	Asp	Ala		
230					235					240					245		
cgt	ccg	gca	act	tgacagccccg	aaaaataaaa	aagacaattt	agaggatgga									888	
Arg	Pro	Ala	Thr														
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atgcagatgt	gtgtgtacat	atgtgtctgg	ctgatgtggt	atagccagaa	agatgagggc											1368	
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<210> 21

<212> DNA

### <213> Artificial Sequence

<223> Northern Blot Probe

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gactgcatca	gctgtgcctc	catctgtgga	cagcacccta	agcaatgtgc	atacttctgt	240
gagaacaagc	tcaggagccc	agtgaacctt	ccaccagagc	tcaggagaca	gcggagtgga	300
gaagttgaaa	acaattcaga	caactcggga	aggtaccaag	gattggagca	cagaggctca	360
gaagcaagtc	cagctctccc	ggggctgaag	ctgagtgcag	atcaggtggc	cctggtctac	420
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### <213> Artificial Sequence

<223> ZC20061

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### <213> Artificial Sequence

<223> Oligonucleotide ZC20062

accgccacca ggaagcacag aggac 25

### <213> Artificial Sequence

<223> Northern Blot probe

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 atcagggtctc ctgggcatgg ctaacattga cctggaaaag agcaggactg gtgatgaaat 180  
 tattcttccg agaggcctcg agtacacggt ggaagaatgc acctgtgaag actgcatcaa 240  
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<210> 25  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 25  
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<210> 26  
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 <212> DNA  
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<220>  
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<400> 26  
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<210> 27  
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<220>  
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<400> 27  
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<210> 28  
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<400> 28  
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<210> 29  
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<210> 30  
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<210> 31  
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aagttcaagt	agtgatatgg	atgactccac	agaaagggag	cagtcacgcc	ttactttcttg	180
ccttaagaaa	agagaagaaa	tgaaactgaa	ggagtgtgtt	tccatcctcc	cacggaagga	240
aagcccctct	gtccgatcct	caaagacgg	aaagctgctg	gctgcaacct	tgctgctggc	300
actgctgtct	tgctgcctca	cggtggtgtc	tttctaccag	gtggccgccc	tgcaagggga	360
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tcagggtcca	gaagaaacag	tcactcaaga	ctgcttgcaa	ctgattgcag	acagtgaaac	600
accaactata	caaaaaggat	cttacacatt	tgttccatgg	cttctcagct	ttaaaagggg	660
aagtgcccta	gaagaaaaag	agaataaaat	attgggtcaa	gaaactgggt	acttttttat	720
atatggtcag	gttttatata	ctgataagac	ctacgccatg	ggacatctaa	ttcagaggaa	780
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<400> 37  
gtatacggcg cgcctcacag cagtttcaat gc 32

<210>	38
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<210> 39  
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<212> DNA  
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<223> Oligonucleotide ZC17252

<400> 39

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25

<210> 40

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC17156

<400> 40

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<210> 41

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide ZC17157

<400> 41

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<210> 42

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<212> DNA

<213> Homo sapiens

<400> 42

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cgggggccac	gaaggccact	gcaaaccttg	gacagactgc	accagttcg	ggtttctcac	420
tgtgttccct	gggaacaaga	cccacaacgc	tgtgtgcgtc	ccagggtccc	cgccggcaga	480
gccgcttggg	tggctgaccg	tcgtcctcct	ggccgtggcc	gcctgcgtcc	tcctcctgac	540
ctcgccccag	cttgactgc	acatctggca	gctgaggagt	cagtgcattg	ggccccgaga	600
gaccagctg	ctgctggagg	tgccgccgct	gaccgaagac	gccagaagct	gccagttccc	660
cgaggaagag	cggggcgagc	gatcggcaga	ggagaagggg	cggctgggag	acctgtgggt	720

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<210> 44  
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<213> Homo sapiens

<220>

<221> CDS  
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<223> Ig Fc sequence

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ggatcc atg aag cac ctg tgg ttc ttc ctc ctg ctg gtg gcg gct ccc 48  
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro  
1 5 10

aga tgg gtc ctg tcc gag ccc aga tct tca gac aaa act cac aca tgc 96  
Arg Trp Val Leu Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys  
15 20 25 30

004355-01000





<210> 49  
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<220>  
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<210> 50  
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<220>  
 <223> Oligonucleotide ZC15518

<400> 50  
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<210> 51  
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<220>  
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<210> 52  
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<220>  
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<210> 53

### <213> Artificial Sequence

<223> Oligonucleotide primer

48

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<223> Oligonucleotide primer

59

### <213> Artificial Sequence

<223> Oligonucleotide primer

59

### <213> Artificial Sequence

<223> Oligonucleotide primer

60

<211> 56



<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 57

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<210> 58

<211> 59

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer

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<220>

<223> Antibody peptide

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Ser	Ala	Gly	Ile	Ala	Lys	Leu	Glu	Glu	Gly	Pro	Glu	Leu	Gln	Leu	Ala
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Ile	Pro	Arg	Glu												
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<210> 60

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Antibody peptide

<400> 60

Ser	Phe	Lys	Arg	Gly	Ser	Ala	Leu	Glu	Glu	Lys	Glu	Asn	Lys	Glu	Leu
1					5					10				15	

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